SEQUENCE LISTING

<110> Gray, Joe W
       Collins, Collin
       Hwang, Soo In
       Godfrey, Tony
       Kowel, David
       Rommens, Johanna

<120> GENES FROM THE 20Q13 AMPLICON AND THEIR USES

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<140> 08/892,695
<141> 1997-07-15

<150> 08/785,532
<151> 1997-01-17

<150> 08/731,499
<151> 1996-10-16

<150> 08/680,395
<151> 1996-07-15

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<170> PatentIn Ver. 2.0

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1

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cttccagtat aggaaaccta agatacctag agcggctttt gggaacaatg ggctcatgcc 660
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<223> N is A, G, G, T, or U

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<213> Artificial Sequence

<220>
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<400> 4

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4

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<212> DNA
<213> Artificial Sequence

<220>
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5

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<220>
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<222> (916)
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<220>
<221> modified_base
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<222> (57)
<223> n is A, C, G, T, or U

<220>
<221> modified_base
<222> (449)

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<220>
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7

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10

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tctttgagta aagtttgat tccaagtatc acctgtccat tttgtacctt caagacattt 2160
tatccagaag ttttaatgat gcaccagaga ctggagcata aatacaatcc tgacgttcat 2220
aaaaactgtc gaaacaagtc cttgcttaga agtcgacgta ccggatgccc gccagcgttg 2280
ctgggaaaag atgtgcctcc cctctctagt ttctgtaaac ccaagcccaa gtctgctttc 2340
ccggcgcagt ccaaatccct gccatctgcg aaggggaagc agagccctcc tgggccaggc 2400
aaggcccctc tgacttcagg gatagactct agcactttag ccccaagtaa cctgaagtcc 2460
cacagaccac agcagaatgt ggggtccaa ggggccgcca ccaggcaaca gcaatctgag 2520
atgtttccta aaccagtgt ttcccctgca ccggataaga caaaaagacc cgagacaaaa 2580
ttgaaacctc ttccagtagc tccttctcag cccacccctcg gcagcagtaa catcaatggt 2640
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tgtaatcgga gtgccagcaa tactgcagca gaatttggtg agccccttcc aaaaagactg 2760
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gaccttccca gtaccatat ggtcagaggc atcacatcac tgttaccgca ggactgtgtg 2880
tatccgtcgc aggcgctgcc tcccaaacca aggttcctga gctccagcga ggtcgattct 2940
ccaaatgtgc tgactgttca gaagccctat ggtggctccg gccacttta cacttgtgtg 3000
cctgctggta gtccagcatc cagctcgacg ttagaaggtc ttggtggatg tcagtgctta 3060
ctccccatga aattaaattt tacttcatcc tttgagaagc gaatggtgaa agctactgaa 3120
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gtgtaa                                                           3186
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<210> 11
<211> 1061
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ZABC1 Protein

<400> 11

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Met Gln Ser Lys Val Thr Gly Asn Met Pro Thr Gln Ser Leu Leu Met
 1               5                  10                  15

Tyr Met Asp Gly Pro Glu Val Ile Gly Ser Ser Leu Gly Ser Pro Met
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11

```
                        20                      25                      30

        Glu Met Glu Asp Ala Leu Ser Met Lys Gly Thr Ala Val Val Pro Phe
                35                      40                      45

        Arg Ala Thr Gln Glu Lys Asn Val Ile Gln Ile Glu Gly Tyr Met Pro
                50                      55                      60

        Leu Asp Cys Met Phe Cys Ser Gln Thr Phe Thr His Ser Glu Asp Leu
        65                      70                      75                      80

        Asn Lys His Val Leu Met Gln His Arg Pro Thr Leu Cys Glu Pro Ala
                        85                      90                      95

        Val Leu Arg Val Glu Ala Glu Tyr Leu Ser Pro Leu Asp Lys Ser Gln
                        100                     105                     110

        Val Arg Thr Glu Pro Pro Lys Glu Lys Asn Cys Lys Glu Asn Glu Phe
                        115                     120                     125

        Ser Cys Glu Val Cys Gly Gln Thr Phe Arg Val Ala Phe Asp Val Glu
                130                     135                     140

        Ile His Met Arg Thr His Lys Asp Ser Phe Thr Tyr Gly Cys Asn Met
        145                     150                     155                     160

        Cys Gly Arg Arg Arg Lys Glu Pro Trp Phe Leu Lys Asn His Met Arg
                        165                     170                     175

        Thr His Asn Gly Lys Ser Gly Ala Arg Ser Lys Leu Gln Gln Gly Leu
                        180                     185                     190

        Glu Ser Ser Pro Ala Thr Ile Asn Glu Val Val Gln Val His Ala Ala
                195                     200                     205

        Glu Ser Ile Ser Ser Pro Tyr Lys Ile Cys Met Val Cys Gly Phe Leu
                210                     215                     220

        Phe Pro Asn Lys Glu Ser Leu Ile Glu His Arg Lys Val His Thr Lys
        225                     230                     235                     240

        Lys Thr Ala Phe Gly Thr Ser Ser Ala Gln Thr Asp Ser Pro Gln Gly
                        245                     250                     255

        Gly Met Pro Ser Ser Arg Glu Asp Phe Leu Gln Leu Phe Asn Leu Arg
                        260                     265                     270

        Pro Lys Ser His Pro Glu Thr Gly Lys Lys Pro Val Arg Cys Ile Pro
                275                     280                     285

        Gln Leu Asp Pro Phe Thr Thr Phe Gln Ala Trp Gln Leu Ala Thr Lys
                290                     295                     300

        Gly Lys Val Ala Ile Cys Gln Glu Val Lys Glu Ser Gly Gln Glu Gly
        305                     310                     315                     320

        Ser Thr Asp Asn Asp Asp Ser Ser Ser Glu Lys Glu Leu Gly Glu Thr


                                        12
```

```
                              325                   330                   335
Asn Lys Gly Ser Cys Ala Gly Leu Ser Gln Glu Lys Glu Lys Cys Lys
        340             345             350

His Ser His Gly Glu Ala Pro Ser Val Asp Ala Asp Pro Lys Leu Pro
        355             360             365

Ser Ser Lys Glu Lys Pro Thr His Cys Ser Glu Cys Gly Lys Ala Phe
370             375             380

Arg Thr Tyr His Gln Leu Val Leu His Ser Arg Val His Lys Lys Asp
385             390             395             400

Arg Arg Ala Gly Ala Glu Ser Pro Thr Met Ser Val Asp Gly Arg Gln
            405             410             415

Pro Gly Thr Cys Ser Pro Asp Leu Ala Ala Pro Leu Asp Glu Asn Gly
            420             425             430

Ala Val Asp Arg Gly Glu Gly Gly Ser Glu Asp Gly Ser Glu Asp Gly
        435             440             445

Leu Pro Glu Gly Ile His Leu Asp Lys Asn Asp Asp Gly Gly Lys Ile
        450             455             460

Lys His Leu Thr Ser Ser Arg Glu Cys Ser Tyr Cys Gly Lys Phe Phe
465             470             475             480

Arg Ser Asn Tyr Tyr Leu Asn Ile His Leu Arg Thr His Thr Gly Glu
            485             490             495

Lys Pro Tyr Lys Cys Glu Phe Cys Glu Tyr Ala Ala Ala Gln Lys Thr
        500             505             510

Ser Leu Arg Tyr His Leu Glu Arg His His Lys Glu Lys Gln Thr Asp
        515             520             525

Val Ala Ala Glu Val Lys Asn Asp Gly Lys Asn Gln Asp Thr Glu Asp
        530             535             540

Ala Leu Leu Thr Ala Asp Ser Ala Gln Thr Lys Asn Leu Lys Arg Phe
545             550             555             560

Phe Asp Gly Ala Lys Asp Val Thr Gly Ser Pro Pro Ala Lys Gln Leu
            565             570             575

Lys Glu Met Pro Ser Val Phe Gln Asn Val Leu Gly Ser Ala Val Leu
            580             585             590

Ser Pro Ala His Lys Asp Thr Gln Asp Phe His Lys Asn Ala Ala Asp
        595             600             605

Asp Ser Ala Asp Lys Val Asn Lys Asn Pro Thr Pro Ala Tyr Leu Asp
        610             615             620

Leu Leu Lys Lys Arg Ser Ala Val Glu Thr Gln Ala Asn Asn Leu Ile
```

13

```
         625                    630                    635                    640

    Cys Arg Thr Lys Ala Asp Val Thr Pro Pro Pro Asp Gly Ser Thr Thr
                    645                 650                 655

    His Asn Leu Glu Val Ser Pro Lys Glu Lys Gln Thr Glu Thr Ala Ala
                    660                 665                 670

    Asp Cys Arg Tyr Arg Pro Ser Val Asp Cys His Glu Lys Pro Leu Asn
                    675                 680                 685

    Leu Ser Val Gly Ala Leu His Asn Cys Pro Ala Ile Ser Leu Ser Lys
                    690                 695                 700

    Ser Leu Ile Pro Ser Ile Thr Cys Pro Phe Cys Thr Phe Lys Thr Phe
    705                 710                 715                 720

    Tyr Pro Glu Val Leu Met Met His Gln Arg Leu Glu His Lys Tyr Asn
                    725                 730                 735

    Pro Asp Val His Lys Asn Cys Arg Asn Lys Ser Leu Leu Arg Ser Arg
                    740                 745                 750

    Arg Thr Gly Cys Pro Pro Ala Leu Leu Gly Lys Asp Val Pro Pro Leu
                    755                 760                 765

    Ser Ser Phe Cys Lys Pro Lys Pro Lys Ser Ala Phe Pro Ala Gln Ser
                    770                 775                 780

    Lys Ser Leu Pro Ser Ala Lys Gly Lys Gln Ser Pro Pro Gly Pro Gly
    785                 790                 795                 800

    Lys Ala Pro Leu Thr Ser Gly Ile Asp Ser Ser Thr Leu Ala Pro Ser
                    805                 810                 815

    Asn Leu Lys Ser His Arg Pro Gln Gln Asn Val Gly Val Gln Gly Ala
                    820                 825                 830

    Ala Thr Arg Gln Gln Gln Ser Glu Met Phe Pro Lys Thr Ser Val Ser
                    835                 840                 845

    Pro Ala Pro Asp Lys Thr Lys Arg Pro Glu Thr Lys Leu Lys Pro Leu
        850                 855                 860

    Pro Val Ala Pro Ser Gln Pro Thr Leu Gly Ser Ser Asn Ile Asn Gly
    865                 870                 875                 880

    Ser Ile Asp Tyr Pro Ala Lys Asn Asp Ser Pro Trp Ala Pro Pro Gly
                    885                 890                 895

    Arg Asp Tyr Phe Cys Asn Arg Ser Ala Ser Asn Thr Ala Ala Glu Phe
                    900                 905                 910

    Gly Glu Pro Leu Pro Lys Arg Leu Lys Ser Ser Val Val Ala Leu Asp
                    915                 920                 925

    Val Asp Gln Pro Gly Ala Asn Tyr Arg Arg Gly Tyr Asp Leu Pro Lys
```

```
                  930                     935                     940

      Tyr His Met Val Arg Gly Ile Thr Ser Leu Leu Pro Gln Asp Cys Val
      945                     950                     955                     960

      Tyr Pro Ser Gln Ala Leu Pro Pro Lys Pro Arg Phe Leu Ser Ser Ser
                              965                     970                     975

      Glu Val Asp Ser Pro Asn Val Leu Thr Val Gln Lys Pro Tyr Gly Gly
                              980                     985                     990

      Ser Gly Pro Leu Tyr Thr Cys Val Pro Ala Gly Ser Pro Ala Ser Ser
                    995                    1000                    1005

      Ser Thr Leu Glu Gly Leu Gly Gly Cys Gln Cys Leu Leu Pro Met Lys
                   1010                    1015                    1020

      Leu Asn Phe Thr Ser Ser Phe Glu Lys Arg Met Val Lys Ala Thr Glu
      1025                    1030                    1035                    1040

      Ile Ser Cys Asp Cys Thr Val His Lys Thr Tyr Glu Glu Ser Ala Arg
                             1045                    1050                    1055

      Asn Thr Thr Val Val
                1060


      <210> 12
      <211> 3066
      <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Description of Artificial Sequence:1b1

      <400> 12
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      aagctggagc tccaccgcgg tggcggccgc tctagaacta gtggatcccc cgggctgcag 120
      gaattcggca cgaggctcca ccgacagcca ggcactgggc agcacgcact ggagacccag 180
      gaccctgtgc aggagcagct ccgggtgaca cgaggggact gaagatactc ccacaggggc 240
      tcagcaggag caatgggtaa ccaaatgagt gttccccaaa gagttgaaga ccaagagaat 300
      gaaccagaag cagagactta ccaggacaac gcgtctgctc tgaacggggt tccagtggtg 360
      gtgtcgaccc acacagttca gcacttagag gaagtcgact tgggaataag tgtcaagacg 420
      gataatgtgg ccacttcttc ccccgagaca acggagataa gtgctgttgc ggatgccaac 480
      ggaaagaatc ttgggaaaga ggccaaaccc gaggcaccag ctgctaaatc tcgttttttc 540
      ttgatgctct ctcggcctgt accaggacgt accggagacc aagccgcaga ttcatccctt 600
      ggatcagtga agcttgatgt cagctccaat aaagctccag cgaacaaaga cccaagtgag 660
      agctggacac ttccggtggc agctggaccg gggcaggaca cagataaaac cccagggcac 720
      gcccggcccc aagacaaggt cctctctgcc gccagggatc ccacgcttct cccacctgag 780
      acagggggag caggaggaga agctccctcc aagcccaagg actccagctt ttttgacaaa 840
      ttcttcaagc tggacaaggg acaggaaaag gtgccaggtg acagccaaca ggaagccaag 900
      agggcagagc atcaagacaa ggtggatgag gttcctggct atcagggca gtccgatgat 960
      gtccctgcag ggaaggacat agttgacggc aaggaaaaag aaggacaaga acttggaact 1020
      gcggattgct ctgtccctgg gacccagaa ggactggaga ctgcaaagga cgattcccag 1080
      gcagcagcta tagcagagaa taataattcc atcatgagtt tctttaaaac tctggtttca 1140
      cctaacaaag ctgaaacaaa aaaggaccca gaagacacgg gtgctgaaaa gtcacccacc 1200
      acttcagctg accttaagtc agacaaagcc aactttacat cccaggagac ccaaggggct 1260


                                          15
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ggcaagaatt ccaaaggatg caacccatcg gggcacacac agtccgtgac aacccctgaa 1320
cctgcgaagg aaggcaccaa ggagaaatca ggacccacct ctctgcctct gggcaaactg 1380
ttttggaaaa agtcagttaa agaggactca gtccccacag gtgcggagga gaatgtggtg 1440
tgtgagtcac cagtagagat tataaagtcc aaggaagtag aatcagcctt acaaacagtg 1500
gacctcaacg aaggagatgc tgcacctgaa cccacagaag cgaaactcaa aagagaagaa 1560
agcaaaccaa gaacctctct gatggcgttt ctcagacaaa tgtcagtgaa aggggatgga 1620
gggatcaccc actcagaaga aataaatggg aaagactcca gctgccaaac atcagactcc 1680
acagaaaaga ctatcacacc gccagagcct gaaccaacag gagcaccaca gaagggtaaa 1740
gagggctcct cgaaggacaa gaagtcagca gccgagatga acaagcagaa gagcaacaag 1800
caggaagcca aagaaccagc ccagtgcaca gagcaggcca cggtggacac gaactcactg 1860
cagaatgggg acaagctcca aaagagacct gagaagcggc agcagtccct tgggggcttc 1920
tttaaaggcc tgggaccaaa gcggatgttg gatgctcaag tgcaaacaga cccagtatcc 1980
atcggaccag ttggcaaacc caagtaaaca aatcagcacg gttcccacca ggttctcctg 2040
ccaccaagat gtgttctcct tactccatct cctccccaaa cacgctccat gtatatattc 2100
ttctgatggc cagcaaatga aattctgcct agaaattaag cccgagctgt tgtatattga 2160
ggtgtattat ttacgtctct ggtccagtct tttctggcaa ataacagtaa agatggttta 2220
gcaggtcacc tagttgggtc agaagagtcg atgatcacca agcaggaaag ggagggaata 2280
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gcctgtaatc tcagcacttt gggaggccga ggcaggtgga tcacctgagg tcaggagttc 2400
aagactagcc tggccaacat catgaaaccc cgtctctact aaaaatacaa aaattagcca 2460
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tgtacccagg aggtggaggt tgcagtgagc cgaagttgca ccattgcact ccaccctggg 2580
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tgctgctaga aggaattaag cgttgtagta aacgcgtgct catcctctaa gcttgaagaa 2700
gggagacgaa aatccatttg tttaaattca catctcaagg agggagaacc cgggctgtgt 2760
tgggtggttg ccaatttcct agaacggaat gtgtggggta tagaaaaagg aatgaataag 2820
cgttgttttt caaataggt ccttgtaagt tattgatgag agggaaaaga ttgactgggg 2880
agggcttaaa atgatttggg aaaacaattg cttttgaggc tcagtgacaa cggcaaagat 2940
tacaacttaa aaaaaaaaaa aaaaaactc gagactagtt ctctctctct ctcgtgccga 3000
attcgatatc aagcttatcg ataccgtcga cctcgagggg gggcccggta cccaattcgc 3060
cctata                                                              3066
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<210> 13
<211> 939
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Genomic
      Sequence from BAC Clone 97 Filtered Query Sequence

<220>
<221> modified_base
<222> (191)
<223> n is A, C, G, T, or U

<220>
<221> modified_base
<222> (210)
<223> n is A, C, G, T, or U

<220>
<221> modified_base
<222> (258)
<223> n is A, C, G, T, or U

<220>

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<221> modified_base
<222> (371)
<223> n is A, C, G, T, or U

<220>
<221> modified_base
<222> (418)..(514)
<223> n is A, C, G, T, or U

<220>
<221> modified_base
<222> (416)
<223> n is A, C, G, T, or U

<220>
<221> modified_base
<222> (536)
<223> n is A, C, G, T, or U

<220>
<221> modified_base
<222> (819)..(934)
<223> n is A, C, G, T, or U

<400> 13
tgtgatattg attcatgccc tcttgcacct tgccaaacat cacacgcttg ccatccagtc 60
cactcgattt tggcagtgca gatgaaaaac tgggaaccat ttgtgttgag tccagcaaga 120
tgccaggacc tgcatgtttc agaacgaagt tcttcatcat ccaatttctc cctgtatatg 180
ggcttaccac nactgccgtt aagtcgtgtn aagtcaccac tcaggtacat aatggaataa 240
ttctgcaaag gcaggagnca ctttctctcc agtgctcaga ccatgaaagt tttctgatgt 300
ctttggaact ttgtctgcaa atagctcgaa ggagacatgg cctaaaggct cgccatctgc 360
ggtgatattg naacatggta gggctgaccg tggctgtggc catgactttt tagantnnnn 420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnncccaat gcgggacaga gaatcnaaga 540
aactgtatta gggaaagggt cctgagttta tgccaaagtt tcccagattg gtttccattg 600
aaacgtagct ctgtgagata ccatcaggtg ttatgtgaag aaatgtctgt gtagtcaaat 660
atgtttgagt gagtgagcct gagctgagca agactttact gcaagacttc ccatcttctg 720
tccctttta tgctaatggg taacacaaac tccaaaagtg gggtgtacag catgaggcat 780
taacaaaaat ttattggacc ccacacacnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 840
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 900
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnctctc 939

<210> 14
<211> 112
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Subject Seq -
      Rat Cyclophillin 64-175

<400> 14
ttcgacatca cggctgatgg cgagcccttg ggtcgcgtct gcttcgagct gtttgcagac 60
aaagttccaa agacagcaga aaactttcgt gctctgagca ctggggagaa ag 112

<210> 15
<211> 106
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17

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:e:Subject Seq -
      Rat Cyclophilli404-348

<400> 15
tgctggacca aacacaaatg gttcccagtt ttttatctgc actgccaaga ctgagtgggg 60
ctggatggca agcatgtggt ctttgggaag gtgaaagaag gcatga                106

<210> 16
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:e:Subject Seq -
      Rat Cyclophillin 299-336

<400> 16
agaacttcat cctgaagcat acaggtcctg gcatcttg                         38

<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:e:Subject Seq -
      Rat Cyclophillin 193-220

<400> 17
tcctcctttc acagaattat tccaggat                                   28

<210> 18
<211> 112
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Query Seq ID NO
      13 261-372

<220>
<221> modified_base
<222> (2)
<223> n is A, C, G, T, or U

<400> 18
tncaatatca ccgcagatgg cgagccttta ggccatgtct ccttcgagct atttgcagac 60
aaagttccaa agacatcaga aaactttcat ggtctgagca ctggagagaa ag         112

<210> 19
<211> 106
<212> DNA
<213> Artificial Sequence
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18

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<220>
<223> Description of Artificial Sequence:Query Seq ID NO
      13 13-117

<400> 19
tgctggactc aacacaaatg gttcccagtt tttcatctgc actgccaaaa tcgagtggga 60
ctggatggca agcgtgtgat gtttggcaag gtgcaagagg gcatga              106

<210> 20
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Query Seq ID NO
      13116-153

<400> 20
agaacttcgt tctgaaacat gcaggtcctg gcatcttg                       38

<210> 21
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Query Seq ID NO
      13 229-256

<400> 21
tcctgccttt gcagaattat tccattat                                  28

<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward primer

<400> 22
ttggcattgg tatcaggtag ctg                                       23

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 23
ttggagcaga gaggggattg tgtg                                      24

<210> 24
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```
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:: Forward
      primer

<400> 24
aatcccctca aaccctgctg ctac                                    24

<210> 25
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 25
tggagcctga acttctgcaa tc                                      22

<210> 26
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:: Forward
      primer

<400> 26
ccgggatacc gacattg                                           17

<210> 27
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 27
tgcacataaa acagccagc                                         19

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:: Forward
      primer

<400> 28
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ttggaatcaa tggagcaaaa   20

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
     Primer

<400> 29
agctttaccc aatgtggtcc   20

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:: Forward
     primer

<400> 30
gtggtgaaca ccaataaatg g   21

<210> 31
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
     Primer

<400> 31
aagcaaataa aaccaataaa ctcg   24

<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:: Forward
     primer

<400> 32
caagatctga ccccgtcaat c   21

<210> 33
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward

Primer

<400> 33
gacttcttca ggaaagagat cagtg   25

<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:: Forward
      primer

<400> 34
gccatgtacc cacctgaaaa atc   23

<210> 35
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 35
tcagaacacc cgtgcagaat taag   24

<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:: Forward
      primer

<400> 36
cctaaaactt ggtgcttaaa tcta   24

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 37
gtctcacaag gcagatgtgg   20

<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence

22

<220>
<223> Description of Artificial Sequence:: Forward
      primer

<400> 38
tttgtgtatg ttgagccatc   20

<210> 39
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 39
cttccaatct cattctatga gg   22

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer

<400> 40
gcttgtttaa gtgtcactag gg   22

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 41
cactctggta aatgaccttt gtc   23

<210> 42
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:: Forward
      primer

<400> 42
cctacaccat tccaactttg g   21

<210> 43
<211> 25

23

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 43
gccagatgta tgtttgctac ggaac   25

<210> 44
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:: Forward
      primer

<400> 44
tctcaaacct gtccacttct tg   22

<210> 45
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 45
ctgctgtggt ggagaatgg   19

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:: Forward
      primer

<400> 46
tgtcctcctt ctccctcatc ctac   24

<210> 47
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 47
aatgcctcca ctcacaggaa tg   22

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<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:: Forward
      primer

<400> 48
cctcttcagt gtcttcctat tga                                    23


<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 49
gggaggaggt tgtaggcaac                                        20


<210> 50
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward primer

<400> 50
agcaaagcaa aggtggcaca c                                      21


<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 51
tgacatggga gaagacacac ttcc                                   24


<210> 52
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<220>
<223> Description of Artificial Sequence:Forward Primer

<400> 52
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aggtttacca atgtgtttgg   20

<210> 53
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 53
tctacatccc attctcttct g   21

<210> 54
<211> 21
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<220>
<223> Description of Artificial Sequence:: Forward
      primer

<400> 54
gtggtgaaca ccaataaatg g   21

<210> 55
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<212> DNA
<213> Artificial Sequence   .

<220>
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      Primer

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<220>
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<400> 56
ttggaatcaa tggagcaaaa   20

<210> 57
<211> 20
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<220>
<223> Description of Artificial Sequence: Backward
      Primer

26

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<400> 57
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<210> 58
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer

<400> 58
gccatgtacc cacctgaaaa atc                                23


<210> 59
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Backward
      Primer

<400> 59
tcagaacacc cgtgcagaat taag                               24
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